e show
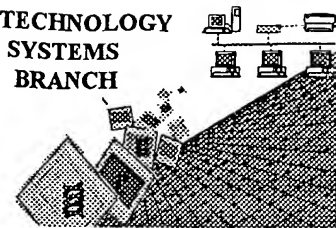
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/603,138*
Source: *O/PE*
Date Processed by STIC: *7/30/2003*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/603,138_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) 8467 missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

RAW SEQUENCE LISTING   DATE: 07/31/2003
PATENT APPLICATION: US/10/603,138   TIME: 07:45:01

Input Set : N:\DA\pto.da.txt
Output Set: N:\CRF4\07312003\J603138.raw

```
  3 <110> APPLICANT: Cathy Lofton-Day
  4         Andrew Sledziewski
  5         Jorn Lewin
  6         Fabian Model
  7         Tamas Rujan
```

pp 1-5

```
  9 <120> TITLE OF INVENTION: Methods and nucleic acids for analyses of colorectal cell
proliferative
 10         disorders.
 12 <130> FILE REFERENCE: 47675-47
```
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/603,138   *result of*
C--> 14 <141> CURRENT FILING DATE: 2003-06-23 *many duplicated sequences)*
E--> 14 <160> NUMBER OF SEQ ID NOS: (8475) 8865 *(many duplicated sequences)*

(see p.5)

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

E--> 31223 <210> SEQ ID NO: 1186 *(see p.2)*
~~E'--> 35524 <210> SEQ ID NO: 1578~~
```
    111365 <210> SEQ ID NO: 8467
    111366 <211> LENGTH: 0
    111367 <212> TYPE: DNA
    111368 <213> ORGANISM: Artificial Sequence
    111370 <220> FEATURE:
    111371 <223> OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
    111373 <400> SEQUENCE: 8467
```
delete all this

E--> 111375   000 *(insert)*

(if the above sequence is intentionally skipped, or delete please use format shown in item 8 of Error Summary Sheet)

```
<210> 1577
<211> 22
<212> DNA
<213> Artificial Sequence

<220> bisulfite treated
<223> nucleic acid for analysis of methylation status of SEQ ID NO: 27
<400> 1577
TATACGCGAT TTACGGTAGA GG                                          22
```

move this to <223> line (do not show any response to <220>)

```
<210> 1186
<211> 22
```

duplicate (already shown in file)

```
<212> DNA
<213> Artificial Sequence

<220> bisulfite treated
```

same error

```
<223> nucleic acid for analysis of methylation status of SEQ ID NO: 4
<400> 1186
AGTTTCGCGG TTTATAGAGG TT                                          22
```

```
<210> 1187
<211> 22
```

duplicate (already shown)

(many sequences duplicated)
after 1186 above

This error begins with Sequence 1160 (appears in many subsequent sequences)

<210> 1160
<211> 18
<212> DNA
<213> Artificial Sequence

<220> (bisulfite treated) *move to <2237 line* *do not show any response to <2207. It is a "header" only.*
<223> nucleic acid for analysis of methylation status of SEQ ID NO 16.
<400> 1160

GGTTTCGGTT CGAGGTTC 18

use only lower-case letters for nucleotides, when Sequence Listing is in new Sequence Rules format.

(Please edit all sequence showing upper-case letters for nucleotides)

<210> 536
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Detection primer for what? (This is a sample of global error)

<400> 536

10/603,138   5

<210> 8474   *FYI: last sequence in submitted file, not*
<211> 36   *8475, as*
<212> DNA   *shown on*
<213> Artificial Sequence   *p. 1 in*
                <1607 response
<220>
<223> chemically treated genomic DNA (Homo sapiens)

<400> 8474   36

attaatggtt ttataagacg gattttttt taacgt

FYI Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\07312003\J603138.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:2100
L:11560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:404 after pos.:2100
L:11580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:405 after pos.:60
L:18394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:520 after pos.:2100
L:18414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:521 after pos.:60
L:26628 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26631 M:112 C: (48) String data converted to lower case,
L:26639 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26642 M:112 C: (48) String data converted to lower case,
L:26650 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26653 M:112 C: (48) String data converted to lower case,
L:26661 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26664 M:112 C: (48) String data converted to lower case,
L:26672 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26675 M:112 C: (48) String data converted to lower case,
L:26683 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26686 M:112 C: (48) String data converted to lower case,
L:26694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26697 M:112 C: (48) String data converted to lower case,
L:26705 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26708 M:112 C: (48) String data converted to lower case,
L:26716 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26719 M:112 C: (48) String data converted to lower case,
L:26727 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26730 M:112 C: (48) String data converted to lower case,
L:26738 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26741 M:112 C: (48) String data converted to lower case,
L:26749 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26752 M:112 C: (48) String data converted to lower case,
L:26760 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26763 M:112 C: (48) String data converted to lower case,
L:26771 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26774 M:112 C: (48) String data converted to lower case,
L:26782 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26785 M:112 C: (48) String data converted to lower case,
L:26793 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26796 M:112 C: (48) String data converted to lower case,
L:26804 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26807 M:112 C: (48) String data converted to lower case,
L:26815 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26818 M:112 C: (48) String data converted to lower case,
L:26826 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26829 M:112 C: (48) String data converted to lower case,
L:26837 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26840 M:112 C: (48) String data converted to lower case,
L:26848 M:256 W: Invalid Numeric Header Field, <220> has non-blank data

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\07312003\J603138.raw**

```
L:26851 M:112 C: (48) String data converted to lower case,
L:26859 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26862 M:112 C: (48) String data converted to lower case,
L:26870 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26873 M:112 C: (48) String data converted to lower case,
L:26881 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26884 M:112 C: (48) String data converted to lower case,
L:26892 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26895 M:112 C: (48) String data converted to lower case,
L:26903 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26906 M:112 C: (48) String data converted to lower case,
L:26915 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26918 M:112 C: (48) String data converted to lower case,
L:26926 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26929 M:112 C: (48) String data converted to lower case,
L:26937 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26940 M:112 C: (48) String data converted to lower case,
L:26948 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26951 M:112 C: (48) String data converted to lower case,
L:26959 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26962 M:112 C: (48) String data converted to lower case,
L:26970 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26973 M:112 C: (48) String data converted to lower case,
L:26981 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26984 M:112 C: (48) String data converted to lower case,
L:26992 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:26995 M:112 C: (48) String data converted to lower case,
L:27003 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27006 M:112 C: (48) String data converted to lower case,
L:27014 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27017 M:112 C: (48) String data converted to lower case,
L:27025 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27028 M:112 C: (48) String data converted to lower case,
L:27036 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27039 M:112 C: (48) String data converted to lower case,
L:27047 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27050 M:112 C: (48) String data converted to lower case,
L:27058 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27061 M:112 C: (48) String data converted to lower case,
L:27069 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27072 M:112 C: (48) String data converted to lower case,
L:27080 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27083 M:112 C: (48) String data converted to lower case,
L:27091 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27094 M:112 C: (48) String data converted to lower case,
L:27102 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27105 M:112 C: (48) String data converted to lower case,
L:27113 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27116 M:112 C: (48) String data converted to lower case,
```

Input Set : **N:\DA\pto.da.txt**
Output Set: **N:\CRF4\07312003\J603138.raw**

```
L:27124 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27127 M:112 C: (48) String data converted to lower case,
L:27135 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27138 M:112 C: (48) String data converted to lower case,
L:27146 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27149 M:112 C: (48) String data converted to lower case,
L:27157 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27160 M:112 C: (48) String data converted to lower case,
L:27168 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:27171 M:112 C: (48) String data converted to lower case,
L:31223 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 1186
L:35524 M:214 E: (33) Seq.# missing, SEQ ID NO:1577
L:111375 M:301 E: (44) No Sequence Data was Shown, SEQ ID:8467
L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (8475) Counted (8865)
```